

**IN THE SPECIFICATION**

Please replace the paragraph beginning on line 31, page 9 of the specification with the following paragraph:

The MmeI endonuclease was cloned New England Biolabs, Inc. (Beverly, MA) and its amino acid sequence was determined (U.S. Application Publication No. US-2004-0091911-A1, filed concurrently herewith, the disclosure of which is herein incorporated by reference). A BLAST search of the Genbank database using the MmeI endonuclease amino acid sequence as the query returned a number of sequences that were highly significantly similar to MmeI. Among these was a sequence, GenBank accession #AAG03371, which encoded a gene labeled gcrY, and annotated as a "hypothetical 107.5 kDa protein". This hypothetical protein was encoded on a 51,409 base pair plasmid isolated from *Corynebacterium striatum* M82B (see Tauch,A., Krieft,S., Kalinowski,J. and Puhler,A., "The 51,409-bp R-plasmid pTP10 from the multiresistant clinical isolate *Corynebacterium striatum* M82B is composed of DNA segments initially identified in soil bacteria and in plant, animal, and human pathogens" *Mol. Gen. Genet.* 263 (1), 1-11 (2000)). A sample of this plasmid DNA was kindly provided by the author, Andreas Tauch. The DNA sequence encoding and flanking the potential endonuclease gene was known. Primers were designed to specifically amplify the gene from *Corynebacterium striatum* M82B DNA, with convenient restriction enzyme sites added to facilitate cloning into a vector. The amplified gene was inserted into an

expression vector and cloned into an *E. coli* host. Transformed host cells were tested and several were found to express an endonuclease activity when incubated in NEBuffer 4 supplemented with 100mM SAM (S-adenosyl-methionine) (Figure 7). The DNA recognition sequence of this new endonuclease was determined by mapping the positions of cleavage in pUC19, pBR322 and PhiX174 DNAs. These locations of cleavage were found to be consistent with the sequence 5'-AAGGAG-3' (or 5'-CTCCTT-3' on the complement DNA strand). This novel enzyme was named CstMI (from *Corynebacterium striatum* M82B). This recognition sequence is quite different from that of MmeI, which recognizes 5'-TCC(Pu)AC-3', even though the enzymes share approximately 40% identical and 51% similar amino acids in their sequences (Figure 86). The point of DNA cleavage relative to the recognition sequence was determined by cutting an appropriate DNA with CstMI, purifying the DNA and subjecting it to standard dideoxy automated sequencing. CstMI was found to cleave DNA at the same position relative to its recognition sequence as MmeI; namely after the 20th nucleotide 3' to the 5'-AAGGAG-3' recognition sequence strand, and before the 18th nucleotide 5' to the 5'-CTCCTT-3' recognition sequence strand, producing a 2 base pair 3' extension. CstMI was also found to in vivo modify the recombinant expression vector, pTBCstMI.3, such that it was protected against CstMI endonuclease activity in vitro.